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APR 23 2003

TECH CENTER



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,876

DATE: 04/16/2003

TIME: 16:55:53

Input Set : A:\EP.txt

Output Set: N:\CRF4\04162003\I715876.raw

3 <110> APPLICANT: Edwards Jr., John E., et al.

5 <120> TITLE OF INVENTION: Pharmaceutical Compositions and Methods to Vaccinate Against

Disseminated

6 Candidiasis.

8 <130> FILE REFERENCE: 13361.4001

10 <140> CURRENT APPLICATION NUMBER: US 09/715,876

11 <141> CURRENT FILING DATE: 2000-11-18

13 <160> NUMBER OF SEQ ID NOS: 8

15 <170> SOFTWARE: PatentIn version 3.0

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 33

19 <212> TYPE: DNA

20 <213> ORGANISM: Artificial sequence

22 <220> FEATURE:

23 <223> OTHER INFORMATION: PCR Primer

25 <400> SEQUENCE: 1

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29 <210> SEQ ID NO: 2

30 <211> LENGTH: 32

31 <212> TYPE: DNA

32 <213> ORGANISM: Artificial sequence

34 <220> FEATURE:

35 <223> OTHER INFORMATION: PCR Primer

37 <400> SEQUENCE: 2

38 ccgctcgagt cactaaatga acaaggacaa ta

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41 <210> SEQ ID NO: 3

42 <211> LENGTH: 31

43 <212> TYPE: DNA

44 <213> ORGANISM: Artificial sequence

46 <220> FEATURE:

47 <223> OTHER INFORMATION: PCR Primer

49 <400> SEQUENCE: 3

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53 <210> SEQ ID NO: 4

54 <211> LENGTH: 31

55 <212> TYPE: DNA

56 <213> ORGANISM: Artificial sequence

58 <220> FEATURE:

59 <223> OTHER INFORMATION: PCR Primer

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65 <210> SEQ ID NO: 5

66 <211> LENGTH: 20

67 <212> TYPE: DNA

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68 <213> ORGANISM: Artificial sequence  
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71 <223> OTHER INFORMATION: PCR Primer  
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77 <210> SEQ ID NO: 6  
78 <211> LENGTH: 22  
79 <212> TYPE: DNA  
80 <213> ORGANISM: Artificial sequence  
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83 <223> OTHER INFORMATION: PCR Primer  
85 <400> SEQUENCE: 6  
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90 <211> LENGTH: 3786  
91 <212> TYPE: DNA  
92 <213> ORGANISM: Candida albicans  
94 <400> SEQUENCE: 7  
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99 aaaggccag gataccaaac ttgaaatgct gtttgggtt ggtccttata tggtaccagt 180  
101 gccaatccag gggatacatt cacattgaat atgccatgtg tgtttaata tactacttca 240  
103 caaacatctg ttgatttaac tgccatgtt gttaaatatg ctacttgc当地 attttattct 300  
105 ggtgaagaat tcacaactt ttctacatata acatgtactg tgaacgacgc tttgaatca 360  
107 tccattaagg catttggta agttacttta ccaattgc当地 tcaatgttgg tggAACAGGT 420  
109 tcatcaactg atttggaaa ttctaaatgtt ttactgtctg gtaccaatac agtcacattt 480  
111 aatgatggta ataaagatat ctcaattgtat gttgatgtt gaaagtcaac cgttgatcca 540  
113 agtgcattt tggatgttcc cagatgtt gcaatgtctca ataaggtcac aactctttt 600  
115 gtggcaccac aatgtgaaaa tgggttacaca tctggtacaa tgggttctc cagtagtaac 660  
117 ggtgacgttg ctattgattt ctcaaatattt catattggta tcacaaaagg attaaatgat 720  
119 tggattttt cggtttccatc tgaatcattt agttacacta aaacttgc当地 atctaattgga 780  
121 attcagatta aatataaaaa tggatgtt ggttacatc当地 catttatttga tgcttatatt 840  
123 tctgctacag atgtaacca atatacttta gcatataacca atgattatac ttgtgctggc 900  
125 agtcgtctgc aaagtaaacc ttctacttta agatggactg gatacaagaa tagtgatgcc 960  
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129 gtcactactt taccatcaa tccaaatgtt gataaaaacca aaacaatcga aattttgcaa 1080  
131 cctattccaa ccactaccat cacaacttca tatgttgggt tgactacttc ctatctgact 1140  
133 aagactgcac caattggta aacagctact gttattgtt atgtgccata tcataactacc 1200  
135 acaactgtta ccagtgaatg gacaggaaca atcactacca ccacaactcg taccatcca 1260  
137 actgattcaa ttgacacagt ggtggtaaa gttccactgc caaatccaaac tgtagtact 1320  
139 actgaatattt ggtctcactt ctttgc当地 accactacag ttactgtctc tccaggtgg 1380  
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143 tcacaatcct ttgctactac tactactgtt actgctccctc caggtggta tgactcagta 1500  
145 attatcagag aaccacaaa tccaaatgtc actacaaccc agtattggtc tcaatcctt 1560  
147 gctactacta ctacaggta tggctccatca ggtggtaactg actcagtaat tattcagagaa 1620  
149 cctccaaacc caactgtcactt caccactgaa tattggccc aatcttacgc aaccacaact 1680  
151 actgtgactg ctcctccagg agggactgac tcagtaattt tcaagagaacc accaaaccac 1740  
153 actgtcacta ctactgaata ctggtcacaa tcatatgcca ccactaccac tggtaactgca 1800  
155 ccaccaggtt gtactgacac tggatgttccatca agagagccac caaaccacac tggtaactact 1860

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159	actgatactg	ttatcattag	ggaaccacca	aacccaactg	tcaccactac	tgaatactgg	1980										
161	tctcaatcat	atgcaaccac	tactaccatt	accgctccac	ctggtaaac	tgataaccgtt	2040										
163	cttatacgag	agccacccaa	ccatactgtc	actactactg	aatactggtc	tcaatcatat	2100										
165	gctacaacca	ccactgttac	tgcaaccac	ggtgaaaccc	ataccgttct	tatcagagag	2160										
167	ccaccaaacc	atactgtcac	tactactgaa	tactggtctc	aatcatatgc	tacaaccacc	2220										
169	actgttactg	caccaccagg	tggtaccgat	actgttatca	ttagagagcc	accaaatcca	2280										
171	acagttacta	ctactgaata	ttggtcacaa	tcatttgc	caaccaccac	agttactgct	2340										
173	cctccaggtg	gtactgacac	tgtgattatc	tatgaaagca	tgtcaagttc	aaagatttct	2400										
175	acatcctcca	atgatataac	cagtatcatt	ccatcattt	cccgctctca	ttatgtcaac	2460										
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179	agtagtgatg	gtatgtgtt	gttcttaca	actttggta	ctgaatcaga	aacaactaca	2580										
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189	ccattatcat	cttcagtgac	atcattgact	cagttgtctt	caattccaag	tgtttcagaa	2880										
191	agtggaaatgt	aagttacatt	tacaagcaat	ggagacaacc	aaagtggatc	tcatgattca	2940										
193	caatctactt	ccactgaaat	tgaaattgt	acaaccagt	ctactaaagt	tttaccac	3000										
195	gtcgtttctt	ctaatactga	tttactgt	gaaccaacaa	ataccagaga	acaaccaact	3060										
197	acattatcaa	ctacttcaaa	ctccatcaact	gaagatatca	ccacatctca	acctacagg	3120										
199	gataatggag	acaatacttc	atcaaccaat	ccagttccaa	ctgtggcaac	aagtacttta	3180										
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234	Ala	Lys	Thr	Ile	Thr	Gly	Val	Phe	Asp	Ser	Phe	Asn	Ser	Leu	Thr	Trp	
235					20				25					30			
237	Ser	Asn	Ala	Ala	Asn	Tyr	Ala	Phe	Lys	Gly	Pro	Gly	Tyr	Pro	Thr	Trp	
238					35				40					45			
240	Asn	Ala	Val	Leu	Gly	Trp	Ser	Leu	Asp	Gly	Thr	Ser	Ala	Asn	Pro	Gly	
241					50				55					60			
243	Asp	Thr	Phe	Thr	Leu	Asn	Met	Pro	Cys	Val	Phe	Lys	Tyr	Thr	Thr	Ser	
244					65				70					75			80
246	Gln	Thr	Ser	Val	Asp	Leu	Thr	Ala	Asp	Gly	Val	Lys	Tyr	Ala	Thr	Cys	

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249	Gln Phe Tyr Ser Gly Glu Glu Phe Thr Thr Phe Ser Thr Leu Thr Cys		
250	100	105	110
252	Thr Val Asn Asp Ala Leu Lys Ser Ser Ile Lys Ala Phe Gly Thr Val		
253	115	120	125
255	Thr Leu Pro Ile Ala Phe Asn Val Gly Gly Thr Gly Ser Ser Thr Asp		
256	130	135	140
258	Leu Glu Asp Ser Lys Cys Phe Thr Ala Gly Thr Asn Thr Val Thr Phe		
259	145	150	155
261	Asn Asp Gly Asp Lys Asp Ile Ser Ile Asp Val Glu Phe Glu Lys Ser		
262	165	170	175
264	Thr Val Asp Pro Ser Ala Tyr Leu Tyr Ala Ser Arg Val Met Pro Ser		
265	180	185	190
267	Leu Asn Lys Val Thr Thr Leu Phe Val Ala Pro Gln Cys Glu Asn Gly		
268	195	200	205
270	Tyr Thr Ser Gly Thr Met Gly Phe Ser Ser Ser Asn Gly Asp Val Ala		
271	210	215	220
273	Ile Asp Cys Ser Asn Ile His Ile Gly Ile Thr Lys Gly Leu Asn Asp		
274	225	230	235
276	Trp Asn Tyr Pro Val Ser Ser Glu Ser Phe Ser Tyr Thr Lys Thr Cys		
277	245	250	255
279	Thr Ser Asn Gly Ile Gln Ile Lys Tyr Gln Asn Val Pro Ala Gly Tyr		
280	260	265	270
282	Arg Pro Phe Ile Asp Ala Tyr Ile Ser Ala Thr Asp Val Asn Gln Tyr		
283	275	280	285
285	Thr Leu Ala Tyr Thr Asn Asp Tyr Thr Cys Ala Gly Ser Arg Leu Gln		
286	290	295	300
288	Ser Lys Pro Phe Thr Leu Arg Trp Thr Gly Tyr Lys Asn Ser Asp Ala		
289	305	310	315
291	Gly Ser Asn Gly Ile Val Ile Val Ala Thr Thr Arg Thr Val Thr Asp		
292	325	330	335
294	Ser Thr Thr Ala Val Thr Thr Leu Pro Phe Asn Pro Ser Val Asp Lys		
295	340	345	350
297	Thr Lys Thr Ile Glu Ile Leu Gln Pro Ile Pro Thr Thr Thr Ile Thr		
298	355	360	365
300	Thr Ser Tyr Val Gly Val Thr Thr Ser Tyr Leu Thr Lys Thr Ala Pro		
301	370	375	380
303	Ile Gly Glu Thr Ala Thr Val Ile Val Asp Val Pro Tyr His Thr Thr		
304	385	390	395
306	Thr Thr Val Thr Ser Glu Trp Thr Gly Thr Ile Thr Thr Thr Thr Thr		
307	405	410	415
309	Arg Thr Asn Pro Thr Asp Ser Ile Asp Thr Val Val Val Gln Val Pro		
310	420	425	430
312	Leu Pro Asn Pro Thr Val Ser Thr Thr Glu Tyr Trp Ser Gln Ser Phe		
313	435	440	445
315	Ala Thr Thr Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Thr Val		
316	450	455	460
318	Ile Ile Arg Glu Pro Pro Asn His Thr Val Thr Thr Glu Tyr Trp		
319	465	470	475
			480

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321 Ser Gln Ser Phe Ala Thr Thr Thr Val Thr Ala Pro Pro Gly Gly  
322 485 490 495  
324 Thr Asp Ser Val Ile Ile Arg Glu Pro Pro Asn Pro Thr Val Thr Thr  
325 500 505 510  
327 Thr Glu Tyr Trp Ser Gln Ser Phe Ala Thr Thr Thr Val Thr Ala  
328 515 520 525  
330 Pro Pro Gly Gly Thr Asp Ser Val Ile Ile Arg Glu Pro Pro Asn Pro  
331 530 535 540  
333 Thr Val Thr Thr Glu Tyr Trp Ser Gln Ser Tyr Ala Thr Thr Thr  
334 545 550 555 560  
336 Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Ser Val Ile Ile Arg Glu  
337 565 570 575  
339 Pro Pro Asn His Thr Val Thr Thr Glu Tyr Trp Ser Gln Ser Tyr  
340 580 585 590  
342 Ala Thr Thr Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Thr Val  
343 595 600 605  
345 Ile Ile Arg Glu Pro Pro Asn His Thr Val Thr Thr Glu Tyr Trp  
346 610 615 620  
348 Ser Gln Ser Phe Ala Thr Thr Thr Val Thr Gly Pro Pro Ser Gly  
349 625 630 635 640  
351 Thr Asp Thr Val Ile Ile Arg Glu Pro Pro Asn Pro Thr Val Thr Thr  
352 645 650 655  
354 Thr Glu Tyr Trp Ser Gln Ser Tyr Ala Thr Thr Thr Ile Thr Ala  
355 660 665 670  
357 Pro Pro Gly Glu Thr Asp Thr Val Leu Ile Arg Glu Pro Pro Asn His  
358 675 680 685  
360 Thr Val Thr Thr Glu Tyr Trp Ser Gln Ser Tyr Ala Thr Thr Thr  
361 690 695 700  
363 Thr Val Thr Ala Pro Pro Gly Glu Thr Asp Thr Val Leu Ile Arg Glu  
364 705 710 715 720  
366 Pro Pro Asn His Thr Val Thr Thr Glu Tyr Trp Ser Gln Ser Tyr  
367 725 730 735  
369 Ala Thr Thr Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Thr Val  
370 740 745 750  
372 Ile Ile Arg Glu Pro Pro Asn Pro Thr Val Thr Thr Glu Tyr Trp  
373 755 760 765  
375 Ser Gln Ser Phe Ala Thr Thr Thr Val Thr Ala Pro Pro Gly Gly  
376 770 775 780  
378 Thr Asp Thr Val Ile Ile Tyr Glu Ser Met Ser Ser Ser Lys Ile Ser  
379 785 790 795 800  
381 Thr Ser Ser Asn Asp Ile Thr Ser Ile Ile Pro Ser Phe Ser Arg Pro  
382 805 810 815  
384 His Tyr Val Asn Ser Thr Thr Ser Asp Leu Ser Thr Phe Glu Ser Ser  
385 820 825 830  
387 Ser Met Asn Thr Pro Thr Ser Ile Ser Ser Asp Gly Met Leu Leu Ser  
388 835 840 845  
390 Ser Thr Thr Leu Val Thr Glu Ser Glu Thr Thr Glu Leu Ile Cys  
391 850 855 860  
393 Ser Asp Gly Glu Cys Ser Arg Leu Ser Ser Ser Gly Ile Val

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### Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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